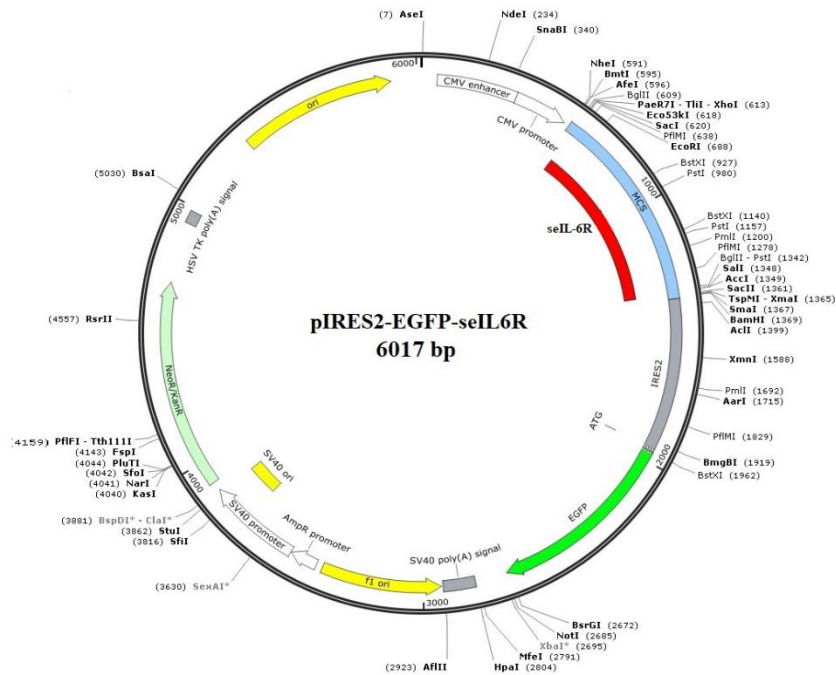
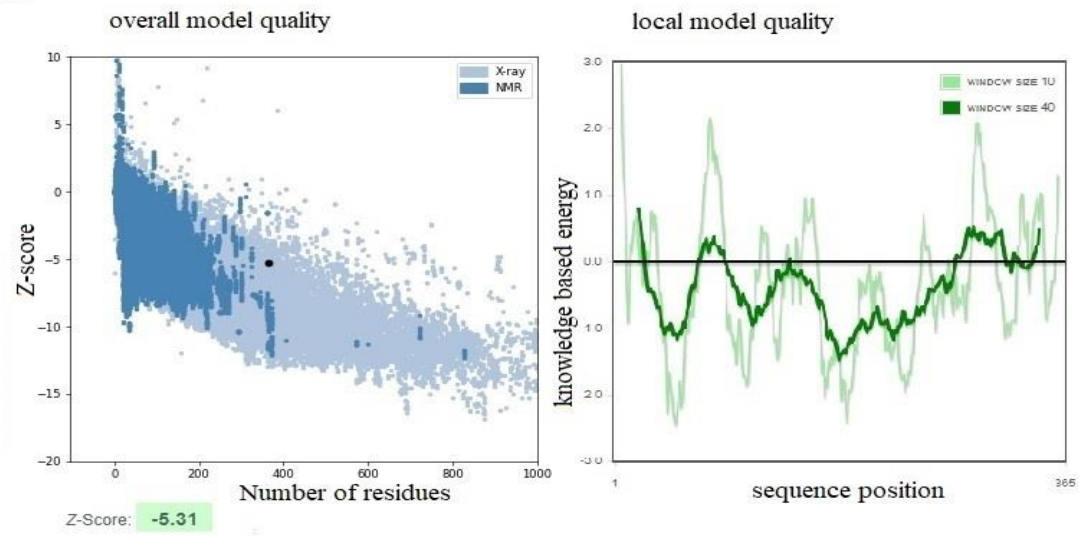
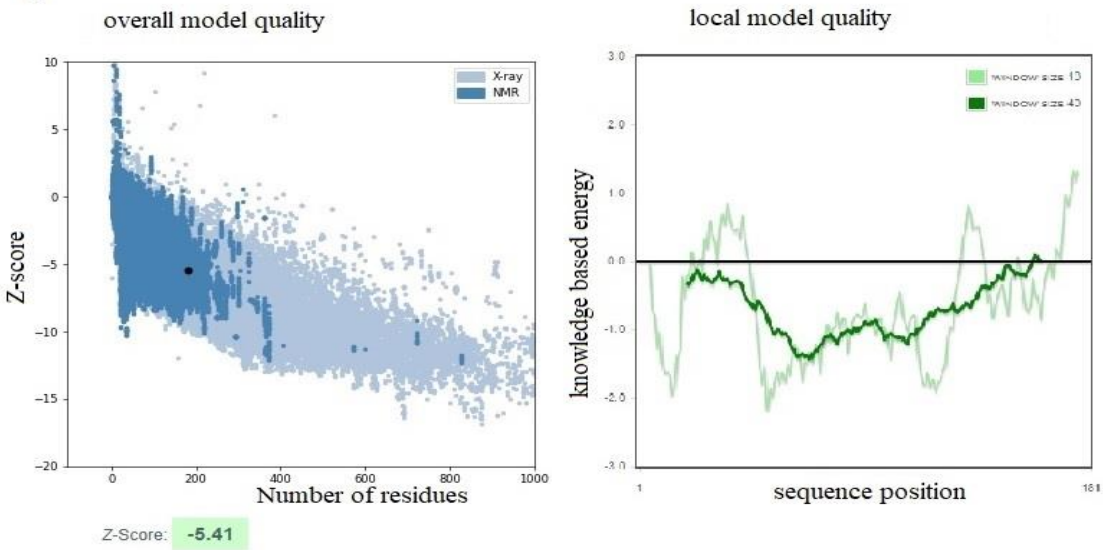




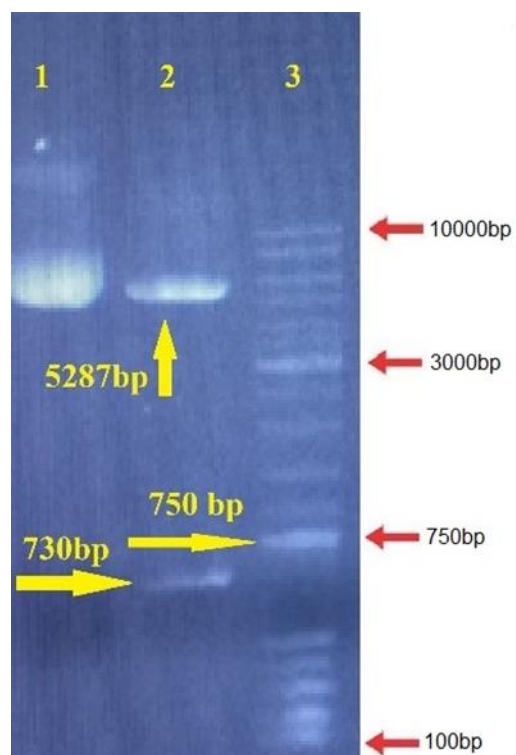
Suppl. 1. Schematic presentation of the pIRES2-EGFP-seIL-6R plasmid. The designed fragment (red color) was designed between *SacI* and *SalI* restriction sites under the CMV promoter. The plasmid has EGFP gene (green color) as an expression marker, a kanamycin-resistant gene for bacterial selection and a Neomycin-resistant gene for selection in the eukaryotic cells.

>seIL-6R 738bp

gagctcgggtaccGCCACCATGGAGTGGGTAACCTTTATTTCCCTTCTTTTCTCTTTAGCTCGGCTTATTCCgaattc
 ATGTGCTTCAGGAAGAGCCCCCTGAGCAACGTGGTGTGCGAGTGGGGCCCCAGGAGCACCCCCAGCCTGA
 CCACCAAGGCCGTGCTGCTGGTGAAGTTCAGAACAGCCCCGCCGAGGACTTCCAGGAGCCCTGCCA
 GTACAGCCAGGAGAGCCAGAAGTTCAGCTGCCAGCTGGCCGTGCCCCAGGGCGACAGCAGCTTCTACATC
 GTGAGCATGTGCGTGGCCAGCAGCGTGGGCAGCAAGTTCAGCAAGACCCAGACCTTCCAGGGCTGCGGCA
 TCCTGCAGCCCCGACCCCCCGCCAACATCACCGTGACCGCCGTGGCCAGGAACCCCAGGTGGCTGAGCGT
 GACCTGGCAGGACCCCCACAGCTGGAACAGCAGCTTCTACAGGCTGAGGTTGAGCTGAGGTACAGGGCC
 GAGAGGAGCAAGACCTTACCACCTGGATGGTGAAGGACCTGCAGCACCACTGCGTGATCCACGACGCCT
 GGAGCGGCCTGAGGCACGTGGTGCAGCTGAGGGCCAGGAGGAGTTCGGCCAGaagcttAAAGAAACCGCT
 GCTGCTAAATTGGAACGCCAGCACATGGACAGCTGAAATAAAGCAATAGCATCACAATTTTCAAAATAAAG
 CATTTTTTTTCACTGCagatctgtcgac

a**b**

Suppl. 4. ProSA validation. (a) IL-6R; (b) seIL-6R. Both of proteins are in the range for native proteins



Suppl. 5. Restriction analysis. Digestion of plasmid with BglII ; 1) Undigested plasmid; 2) Digested plasmid and 3) 10kb DNA Ladder.

Suppl.6 The principal FTIR peaks for the seIL-6R protein.

Peak Number	X (cm-1)	Y (%T)
1	3414.36	90.2
2	1618.15	102.82
3	1410.84	114.43
4	1187.56	111.05
5	1044.84	113
6	591.87	120.17

Suppl. 7 Characteristics infrared bands of peptide linkage.

Designation	Approximate (cm-1)	wavenumber	Description
Amide A	3300		NH stretching
Amide B	3100		NH stretching
Amide I	1600 – 1690		C=O stretching
Amide II bending	1480 – 1575		CN stretching, NH
Amide III	1229 – 1301		CN stretching, NH bending
Amide IV	625 – 767		OCN bending
Amide V	640 – 800		Out-of-plane NH bending
Amide VI	537 – 606		Out-of-plane C=O bending
Amide VII	200		Skeletal torsion